09/023483

WEST

Freeform Search

Database: US Patents Full-Text Database; US Pre-Grant Publication Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: L7 and total DNA

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

Search | Clear | Help | Logout | Interrupt

Main Menu | Show S Numbers | Edit S Numbers | Preferences | Cases

Search History

DATE: Wednesday, October 23, 2002 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L8	L7 and total DNA	12	L8
L7	L6 and (quantif$ near5 DNA)	95	L7
L6	random near5 primer$1	3221	L6
L5	l1 and (random near5 primer$1)	0	L5
L4	radom near5 primer$1	0	L4
L3	l1 and radom	0	L3
L2	L1 and (radom near5 primer$1)	0	L2
L1	quantif$ near5 total near5 DNA	17	L1

END OF SEARCH HISTORY

Generate Collection | Print

Search Results - Record(s) 1 through 10 of 12 returned.

☐ 1. 6444656 . 24 Mar 00; 03 Sep 02. Antiviral phosphonate nucleotides. Nguyen-Ba; Nghe, et al. 514/81; 514/86 514/88 544/243 544/244. A61K031/525 A61K031/52 C07H009/38.

☐ 2. 6312911 . 05 May 00; 06 Nov 01. DNA-based steganography. Bancroft; Frank Carter, et al. 435/6;. C12Q001/68.

☐ 3. 6242211 . 05 Mar 99; 05 Jun 01. Methods for generating and screening novel metabolic pathways. Peterson; Todd C., et al. 435/41; 435/320.1 435/463 435/468 435/477 435/91.41 435/91.52 536/23.5 536/23.7. C12N015/66 C12N015/90 C12N015/70 C12N015/85 C12N015/12.

☐ 4. 6203977 . 26 Sep 94; 20 Mar 01. Delineation of individual human chromosomes in metaphase and interphase cells by in situ suppression hybridization. Ward; David C., et al. 435/6; 536/24.3 536/27.1. C12Q001/68 C07H021/04.

☐ 5. 5874563 . 05 Jun 95; 23 Feb 99. Hepatitis G virus and molecular cloning thereof. Kim; Jungsuh P., et al. 536/23.72; 435/5 435/69.3 435/91.2 435/91.33 536/24.3 536/24.32. C07H021/04 C07H021/02 C12Q001/70.

☐ 6. 5856134 . 05 Jun 95; 05 Jan 99. Hepatitis G virus and molecular cloning thereof. Kim; Jungsuh P., et al. 435/69.3; 424/189.1. C12P021/02 A61K039/29.

☐ 7. 5849532 . 06 Jun 95; 15 Dec 98. Hepatitis G virus and molecular cloning thereof. Kim; Jungsuh P., et al. 435/69.3; 435/252.3 435/320.1 435/69.1. C12N001/21 C12N001/19.

☐ 8. 5824507 . 19 May 95; 20 Oct 98. Hepatitis G virus and molecular cloning thereof. Kim; Jungsuh P., et al. 435/69.3; 435/5 530/826. C12Q001/70 C12N015/03.

☐ 9. 5824485 . 24 Apr 96; 20 Oct 98. Methods for generating and screening novel metabolic pathways. Thompson; Katie A., et al. 435/6; 435/320.1 435/455 435/471 435/489 435/69.1 435/91.41 435/DIG.23 435/DIG.26 435/DIG.47 435/DIG.5 435/DIG.6 435/DIG.7 435/DIG.8 536/23.1. C12Q001/68 C12P021/02 C12N015/64 C07H021/02.

☐ 10. 5783431 . 24 Oct 96; 21 Jul 98. Methods for generating and screening novel metabolic pathways. Peterson; Todd C., et al. 435/455; 435/320.1 435/463 435/466 435/471 435/472 435/474 435/489 536/23.1. C12N015/64 C07H021/04.

Generate Collection | Print

Term	Documents
TOTAL.DWPI,EPAB,JPAB,USPT.	1199311
TOTALS.DWPI,EPAB,JPAB,USPT.	9321
DNA.DWPI,EPAB,JPAB,USPT.	115419
DNAS.DWPI,EPAB,JPAB,USPT.	13375
(7 AND (TOTAL ADJ DNA)).USPT,JPAB,EPAB,DWPI.	12
(L7 AND TOTAL DNA).USPT,JPAB,EPAB,DWPI.	12

Previous Page Next Page

09/023,483

WEST

Help | Logout | Interrupt

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers | Preferences | Cases

Search Results -

Term	Documents
THERSHOLD.DWPI,EPAB,JPAB,USPT.	177
THERSHOLDS.DWPI,EPAB,JPAB,USPT.	9
AMOUNT.DWPI,EPAB,JPAB,USPT.	2176801
AMT.DWPI,EPAB,JPAB,USPT.	324981
AMTS.DWPI,EPAB,JPAB,USPT.	62694
AMOUNTS.DWPI,EPAB,JPAB,USPT.	632978
DNA.DWPI,EPAB,JPAB,USPT.	115419
DNAS.DWPI,EPAB,JPAB,USPT.	13375
CONTAMINAT$	0
CONTAMINAT.DWPI,EPAB,JPAB,USPT.	43
CONTAMINATABILITY.DWPI,EPAB,JPAB,USPT.	3
(THERSHOLD AMOUNT NEAR5 CONTAMINAT$ NEAR5 DNA).USPT,JPAB,EPAB,DWPI.	0

There are more results than shown above. Click here to view the entire set.

Database:
US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L3

Refine Search

Recall Text | Clear

Search History

DATE: Wednesday, October 23, 2002 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L3	thershold amount near5 contaminat$ near5 DNA	0	L3
L2	L1 and PCR	0	L2
DB=DWPI,USPT,EPAB,JPAB; PLUR=YES; OP=ADJ			
L1	threshold near5 contaminat$ near5 DNA	3	L1

END OF SEARCH HISTORY

09/023,483

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspta1806jxt

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

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 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Apr 08  "Ask CAS" for self-help around the clock
 NEWS  3  Apr 09  BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS  4  Apr 09  ZDB will be removed from STN
 NEWS  5  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS  6  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS  7  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS  8  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS  9  Jun 03  New e-mail delivery for search results now available
 NEWS 10  Jun 10  MEDLINE Reload
 NEWS 11  Jun 10  PCTFULL has been reloaded
 NEWS 12  Jul 02  FOREGE no longer contains STANDARDS file segment
 NEWS 13  Jul 22  USAN to be reloaded July 28, 2002;
                  saved answer sets no longer valid
 NEWS 14  Jul 29  Enhanced polymer searching in REGISTRY
 NEWS 15  Jul 30  NETFIRST to be removed from STN
 NEWS 16  Aug 08  CANCERLIT reload
 NEWS 17  Aug 08  PHARMAMarketLetter(PHARMAML) - new on STN
 NEWS 18  Aug 08  NTIS has been reloaded and enhanced
 NEWS 19  Aug 19  Aquatic Toxicity Information Retrieval (AQUIRE)
                  now available on STN
 NEWS 20  Aug 19  IFIPAT, IFICDB, and IFIUDB have been reloaded
 NEWS 21  Aug 19  The MEDLINE file segment of TOXCENTER has been reloaded
 NEWS 22  Aug 26  Sequence searching in REGISTRY enhanced
 NEWS 23  Sep 03  JAPIO has been reloaded and enhanced
 NEWS 24  Sep 16  Experimental properties added to the REGISTRY file
 NEWS 25  Sep 16  Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 26  Sep 16  CA Section Thesaurus available in CAPLUS and CA
 NEWS 27  Oct 01  CASREACT Enriched with Reactions from 1907 to 1985
 NEWS 28  Oct 21  EVENTLINE has been reloaded

 NEWS EXPRESS  October 14 CURRENT WINDOWS VERSION IS V6.01,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)
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Enter NEWS followed by the item number or name to see news on that specific topic.

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  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *


FILE 'HOME' ENTERED AT 13:26:37 ON 23 OCT 2002

=> file medline caplus biosis
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

FILE 'MEDLINE' ENTERED AT 13:26:52 ON 23 OCT 2002

FILE 'CAPLUS' ENTERED AT 13:26:52 ON 23 OCT 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
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FILE 'BIOSIS' ENTERED AT 13:26:52 ON 23 OCT 2002
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=> threshold (10a)contaminat?
THRESHOLD IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s threshold (10a)contaminat?
L1          275 THRESHOLD (10A) CONTAMINAT?

=> s l1 and PCR
L2           11 L1 AND PCR

=> s l2 and radom primer#
L3            0 L2 AND RADOM PRIMER#

=> dup rem l2
PROCESSING COMPLETED FOR L2
L4             6 DUP REM L2 (5 DUPLICATES REMOVED)

=> d l4 1-6 bib ab

L4   ANSWER 1 OF 6  CAPLUS  COPYRIGHT 2002 ACS          DUPLICATE 1
AN   2002:390062  CAPLUS
TI   Validation of real-time PCR methods for the quantification of
     transgenic contaminations in rape seed
AU   Zeitler, Reinhard; Pietsch, Klaus; Waiblinger, Hans-Ulrich
CS   Bayerisches Landesamt fur Umweltschutz, Gentechisches Uberwachungsalbor,
     Augsburg, D-86179, Germany
SO   European Food Research and Technology (2002), 214(4), 346-351
     CODEN: EFRTFO; ISSN: 1438-2377
PB   Springer-Verlag
DT   Journal
LA   English
AB   At present genetically modified oilseed rape (Brassica napus) is not
     allowed to be cultivated in the countries of the European community.  This
     is because rape seed has to be free of any transgenic material if it is
     destined for growth in the European Community.  However, a new regulation
     is forthcoming that will distinguish seed to be labeled from seed that is
     not to be labeled by a legal threshold value for the content of transgenic
     material.  In this paper real-time PCR methods are described
     that are applicable for the quantification of transgenic contaminants
     after screening and identification anal.  The validation of their
```

quantification is demonstrated for contaminants with resistance to the herbicides Basta and Roundup Ready in samples of conventional rape seed. The limits of quantification were detd. for both systems for 50 copies of the transgenic DNA in the reaction assay (confidence interval lower than 30% at a 95% probability level) corresponding to 0.1% of transgenic DNA in the total amt. of genomic DNA. Results show that the real-time PCRs established are applicable with the GeneAmp sequence detection system (Applied Biosystems) as well as with the Light Cycler (Roche). The methods described in this paper can be used for the assessment of a **contamination** in rape seed according to future **threshold** regulations.

RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2002 ACS
AN 2002:783500 CAPLUS
TI A method to recover Salmonella from compost by IMS-**PCR**
AU Civilini, M.
CS Dipartimento di Scienze degli Alimenti, Universita degli Studi di Udine, Udine, 33100, Italy
SO Developments in Soil Science (2002), 28B(Soil Mineral-Organic Matter-Microorganism Interactions and Ecosystem Health), 239-246
CODEN: DSSCDM; ISSN: 0166-0918
PB Elsevier Science B.V.
DT Journal
LA English
AB In this work, a procedure was optimized to recover Salmonella typhimurium from a vegetable compost after its artificial contamination. A combination of a bacteriol. method, immunomagnetic sepn. (IMS), and polymerase chain reaction (**PCR**) techniques allowed a redn. in the detection time to 30 h, while maintaining high specificity. The lower **threshold** of direct amplification from exts. of **contaminated** compost was 108 salmonellae g-1. To improve the sensitivity, a combination of shortened preenrichment and enrichment procedures were optimized and the growth of S. typhimurium evaluated. Immunomagnetic sepn. using anti-Salmonella Dynabeads permitted the recovery of 30 salmonellae per 50 g of compost, the same value obtained with the traditional microbial method, which takes two days longer. Alternative purifn. methods to reduce org. compd. inhibition of the **PCR** reaction mixt. did not improve Salmonella detection under a threshold of 105 salmonellae g-1.

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 6 MEDLINE DUPLICATE 2
AN 2002294648 MEDLINE
DN 22031199 PubMed ID: 12034542
TI A multiplex **PCR** for the detection of Brucella spp. and Leptospira spp. DNA from aborted bovine fetuses.
AU Richtzenhain Leonardo Jose; Cortez Adriana; Heinemann Marcos Bryan; Soares Rodrigo Martins; Sakamoto Sidnei Miyoshi; Vasconcellos Silvio Arruda; Higa Zenaide Maria Morais; Scarcelli Eliana; Genovez Margareth Elide
CS Department of Preventive Veterinary Medicine and Animal Health, University of Sao Paulo, 05508-900, Brazil.. leonardo@usp.br
SO VETERINARY MICROBIOLOGY, (2002 Jun 20) 87 (2) 139-47.
Journal code: 7705469. ISSN: 0378-1135.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200208
ED Entered STN: 20020530
Last Updated on STN: 20020814
Entered Medline: 20020813

AB Bovine brucellosis and leptospirosis are important causes of bovine abortion around the world. Both diseases can be serologically diagnosed, but many factors may cause false positive and negative results. Direct methods based on bacteriological isolation are usually employed, but they are difficult, time consuming and dangerous. Monoplex polymerase chain reaction (**PCR**) have been successfully described for the detection of Brucella spp. and Leptospira spp. Aiming at improvement in the direct diagnosis, a multiplex **PCR** (mPCR) for the detection of these agents in aborted bovine fetuses is described. The detection **threshold** of the mPCR was evaluated in experimentally **contaminated** bovine clinical samples using a conventional proteinase K/SDS or a boiling-based extraction protocols. The mPCR was applied to two groups of clinical samples: 63 episodes of bovine abortion and eight hamsters experimentally infected with Leptospira interrogans serovar pomona. Adopting microbiological isolation as reference, the test showed a sensitivity of 100% in both groups of clinical samples. Seven samples collected from bovine fetuses were Brucella spp. culture negative but showed positive results in mPCR. Regarding Leptospira spp. detection, similar results were observed in three bovine clinical samples. All hamsters infected with Leptospira were positive in both microbiological culture and mPCR. The boiling extraction protocol showed better results in some clinical samples, probably by the removal of **PCR** inhibitors by heat treatment. The high sensitivity, simplicity and the possibility of detection of both bacteria in a single tube reaction support the use of the mPCR described in the routine diagnosis.

L4 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 3
AN 2000:904569 CAPLUS
DN 134:265687
TI Recovery of Salmonella typhimurium from compost with the IMS-**PCR** method
AU Civilini, Marcello; Venuti, Francesca; De Bertoldi, Marco; Damante, Giuseppe
CS Dipartimento di Scienze degli Alimenti, Universita degli Studi di Udine, Udine, 33100, Italy
SO Waste Management & Research (2000), 18(6), 572-576
CODEN: WMARD8; ISSN: 0734-242X
PB Munksgaard International Publishers Ltd.
DT Journal
LA English
AB In this work a procedure was optimized to recover Salmonella typhimurium from a vegetable compost after its artificial contamination. A combination of a bacteriol. method, immunomagnetic sepn. (IMS) and polymerase chain reaction (**PCR**) techniques allowed a redn. in the detection time to 30 h while maintaining high specificity. The lower **threshold** of direct amplification from exts. of **contaminated** compost was 108 salmonellae g-1. To improve the sensitivity, a combination of shortened pre-enrichment and enrichment procedures was optimized and the growth of S. typhimurium evaluated. Immunomagnetic sepn. using anti-Salmonella Dynabeads permitted the recovery of 30 salmonellae per 50 g of compost, the same value obtained with the traditional microbial method, which takes two days longer. Alternative purifn. methods to reduce org. compd. inhibition of the **PCR** reaction mixt. did not improve Salmonella detection under a threshold of 105 salmonellae g-1.
RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:350255 BIOSIS
DN PREV200100350255
TI Blackleg risk potential of seed potatoes determined by quantification of tuber contamination by the causal agent and Erwinia carotovora subsp. atroseptica: A critical review.

AU Perombelon, M. C. M. (1)
CS (1) Scottish Crop Research Institute, Invergowrie, Dundee, DD2 5DA: mperom@scri.sari.ac.uk UK
SO Bulletin OEPP, (Septembre Decembre, 2000) Vol. 30, No. 3-4, pp. 413-420. print.
ISSN: 0250-8052.
DT Article
LA English
SL English; French; Russian
AB Blackleg is a seed-borne disease of potato caused by the soft rot bacterium Erwinia carotovora subsp. atroseptica in temperate regions. Although most seed stocks are extensively **contaminated**, blackleg incidence is related to seed **contamination** level, the **threshold** level for disease development being about 103 cells of E. c. atroseptica per tuber. Disease control relies primarily on the production and use of 'clean' seed potatoes. This is better achieved by planting seed potatoes with a low contamination level than by certification based on blackleg inspection and rogueing. Testing seed-potato stocks for E. c. atroseptica involves four steps, which have not all been fully evaluated. First, sampling to reflect variation in tuber contamination level. Second, tuber tissue is prepared for testing. Third, determination of numbers of E. c. atroseptica, which can be carried out using a selective diagnostic medium (CVP), immunofluorescence colony staining after immuno-capture of the target bacteria, enzyme-linked immunosorbent assay (ELISA) applied to tuber extract after enrichment and a quantitative polymerase chain reaction (**PCR**) assay. Although all methods have the necessary sensitivity level, they suffer from certain important drawbacks, including reliability, specificity and ease of use. Last, interpretation of contamination results in terms of blackleg risk assessment. These steps are discussed critically as a basis for future studies.

L4 ANSWER 6 OF 6 MEDLINE DUPLICATE 4
AN 97022682 MEDLINE
DN 97022682 PubMed ID: 8869042
TI [A study of the expression of MDR1 gene in solid tumors. Initial results of a multicenter evaluation].
Etude de l'expression du gene MDR1 dans des tumeurs solides. Resultats preliminaires d'une evaluation multicentrique.
AU Chevillard S; Vielh P; Vallidire P; Robert J; Marie J P
CS Institut Curie, Paris, France.
SO BULLETIN DU CANCER, (1996 Aug) 83 (8) 626-33.
Journal code: 0072416. ISSN: 0007-4551.
CY France
DT Journal; Article; (JOURNAL ARTICLE)
(MULTICENTER STUDY)
LA French
FS Priority Journals
EM 199611
ED Entered STN: 19961219
Last Updated on STN: 19961219
Entered Medline: 19961115
AB The results obtained from 12 laboratories, dealing with six identical malignant solid tumors, assessing MDR1 phenotype using molecular techniques and immunohistochemistry have been compared. Moreover, comparisons between results of MDR1 gene expression, quantified by RT-**PCR** or Northern blot analysis from 10 RNA and 10 cDNA samples, were also compared between eight laboratories. Results concerning solid tumors show frequent discrepancies between the results obtained by immunohistochemistry and molecular biology techniques. Moreover, inter-laboratory discrepancies concerning immunohistochemistry techniques are observed, suggesting that the interpretation of staining is critical. Results of RT-**PCR** and Northern blot using RNA and cDNA show that discrepancies are less frequent than those observed using

immunohistochemistry. However, Northern blot is not sensitive enough to be used in routine. The problems encountered using RT-**PCR** are the following: positivity **threshold** level, reproducibility and risks of cross-**contamination**.

```
=> file uspatful
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                    20.62      20.83

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE      TOTAL
                                                       ENTRY    SESSION
CA SUBSCRIBER PRICE                                    -1.86      -1.86

FILE 'USPATFULL' ENTERED AT 13:31:08 ON 23 OCT 2002
CA INDEXING COPYRIGHT (C) 2002 AMERICAN CHEMICAL SOCIETY (ACS)

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 22 Oct 2002 (20021022/PD)
FILE LAST UPDATED: 22 Oct 2002 (20021022/ED)
HIGHEST GRANTED PATENT NUMBER: US6470498
HIGHEST APPLICATION PUBLICATION NUMBER: US2002152530
CA INDEXING IS CURRENT THROUGH 22 Oct 2002 (20021022/UPCA)
ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 22 Oct 2002 (20021022/PD)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Aug 2002
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Aug 2002

>>>  USPAT2 is now available.  USPATFULL contains full text of the     <<<
>>>  original, i.e., the earliest published granted patents or         <<<
>>>  applications.  USPAT2 contains full text of the latest US         <<<
>>>  publications, starting in 2001, for the inventions covered in     <<<
>>>  USPATFULL.  A USPATFULL record contains not only the original     <<<
>>>  published document but also a list of any subsequent              <<<
>>>  publications.  The publication number, patent kind code, and      <<<
>>>  publication date for all the US publications for an invention     <<<
>>>  are displayed in the PI (Patent Information) field of USPATFULL   <<<
>>>  records and may be searched in standard search fields, e.g., /PN, <<<
>>>  /PK, etc.                                                         <<<

>>>  USPATFULL and USPAT2 can be accessed and searched together         <<<
>>>  through the new cluster USPATALL.  Type FILE USPATALL to          <<<
>>>  enter this cluster.                                               <<<
>>>                                                                    <<<
>>>  Use USPATALL when searching terms such as patent assignees,       <<<
>>>  classifications, or claims, that may potentially change from      <<<
>>>  the earliest to the latest publication.                           <<<

This file contains CAS Registry Numbers for easy and accurate
substance identification.

=> s threshold (10a) contaminat?
        221749 THRESHOLD
        220893 CONTAMINAT?
L5         356 THRESHOLD (10A) CONTAMINAT?

=> s l5 and PCR
         33025 PCR
L6           8 L5 AND PCR

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7             8 DUP REM L6 (0 DUPLICATES REMOVED)

=> s l7 and radom
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```
L8            8 S L7
             96 RADOM
L9            0 L8 AND RADOM

=> d l7 1-8 bib ab

L7   ANSWER 1 OF 8  USPATFULL
AN     2002:232517  USPATFULL
TI     Robust system for screening mail for biological agents
IN     Call, Charles J., Albuquerque, NM, UNITED STATES
       Hanczyc, Eric, Renton, WA, UNITED STATES
       Kamholz, Andrew, Seattle, WA, UNITED STATES
PA     MesoSystems Technology, Inc. (U.S. corporation)
PI     US 2002124664      A1   20020912
AI     US 2002-66404      A1   20020201 (10)
RLI    Continuation-in-part of Ser. No. US 2001-775872, filed on 1 Feb 2001,
       PENDING Continuation-in-part of Ser. No. US 1999-265620, filed on 10 Mar
       1999, GRANTED, Pat. No. US 6363800 Continuation-in-part of Ser. No. US
       2001-955481, filed on 17 Sep 2001, PENDING
PRAI   US 2001-337674P     20011113 (60)
DT     Utility
FS     APPLICATION
LREP   LAW OFFICES OF RONALD M. ANDERSON, Suite 507, 600 - 108th Avenue N.E.,
       Bellevue, WA, 98004
CLMN   Number of Claims: 87
ECL    Exemplary Claim: 1
DRWN   37 Drawing Page(s)
LN.CNT 4319
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     Items of mail are rapidly processed in a mail sampling system to
       determine if the mail is contaminated with a chemical or biological
       agent. The mail sampling system maintains a negative pressure in a
       containment chamber and includes a triggering sampler that makes a
       threshold determination regarding possible contamination
       , and a detecting sampler that obtains a sample for more detailed
       analysis in response to a signal from the triggering sampler. A sample
       of particulates collected from an item of mail is either removed for
       analysis or analyzed in the system to identify a contaminating agent.
       Optionally, the system includes an archiving sampler, which archives
       samples for subsequent processing and analysis, and a decontamination
       system, which is activated to decontaminate the mail if needed.

L7   ANSWER 2 OF 8  USPATFULL
AN     2002:166386  USPATFULL
TI     Tolerance of trichothecene mycotoxins in plants through the modification
       of the ribosomal protein L3 gene
IN     Harris, Linda J., Greely, CANADA
       Gleddie, Stephen C., Ottawa, CANADA
PA     Ministry of Agriculture (non-U.S. corporation)
PI     US 2002088022      A1   20020704
AI     US 2000-725957     A1   20001130 (9)
RLI    Continuation-in-part of Ser. No. US 2000-567326, filed on 9 May 2000,
       ABANDONED Continuation of Ser. No. US 1997-909828, filed on 12 Aug 1997,
       GRANTED, Pat. No. US 6060646
DT     Utility
FS     APPLICATION
LREP   ROTHWELL, FIGG, ERNST & MANBECK, P.C., 555 13TH STREET, N.W., SUITE 701,
       EAST TOWER, WASHINGTON, DC, 20004
CLMN   Number of Claims: 23
ECL    Exemplary Claim: 1
DRWN   18 Drawing Page(s)
LN.CNT 908
AB     Fusarium graminearum is a plant pathogen, attacking a wide range of
       plant species including corn (ear and stalk rot), barley, and wheat
```

(head blight). Fusarium epidemics result in millions of dollars of losses in crop revenues. Fusarium graminearum infection in the cereals reduces both grain yield and quality. Mycotoxins are produced by many fungal Fusarium species and thus the grain becomes contaminated with these mycotoxins, such as the trichothecenes. The major trichothecene produced by F. graminearum is deoxynivalenol (abbreviated as DON, also known as vomitoxin). Trichothecenes are potent protein synthesis inhibitors and are quite toxic to humans and livestock. A yeast gene has been identified which confers upon yeast tolerant of the trichothecene, trichodermin. A corresponding plant gene has been prepared, which has been used to transform plants. These transformed plants have an increased resistance to Fusarium infestation.

L7 ANSWER 3 OF 8 USPATFULL
AN 2001:109867 USPATFULL
TI Methods and kits for diagnosing and determination of the predisposition for diseases
IN Feinberg, Andrew P., Lutherville, MD, United States
PI US 2001007749 A1 20010712
AI US 2001-759917 A1 20010112 (9)
RLI Continuation of Ser. No. US 1998-114825, filed on 14 Jul 1998, PENDING
DT Utility
FS APPLICATION
LREP KILPATRICK STOCKTON LLP, 2400 MONARCH TOWER, 3424 PEACHTREE ROAD, NE, ATLANTA, GA, 30326
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 1637
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method and a kit for the purpose of diagnosing a disease or determining the predisposition for a disease by measuring abnormalities in imprinting of a gene or population of genes. The disease that can be diagnosed by the present invention is selected from any disease that is mediated by, or is associated with, a particular gene or combination of genes that are subject to imprinting. According the present invention, the imprinting can be abnormally on or can be abnormally off. In those cases where the particular gene that is being examined is normally imprinted, but in the disease state is abnormally not imprinted, the present invention is designed to detect the "loss of imprinting" (hereinafter "LOI") thereby indicating that the disease may be present.

L7 ANSWER 4 OF 8 USPATFULL
AN 2001:75127 USPATFULL
TI Methods and kits for diagnosing and determination of the predisposition for diseases
IN Feinberg, Andrew P., Lutherville, MD, United States
PA The Johns Hopkins University, Baltimore, MD, United States (U.S. corporation)
PI US 6235474 B1 20010522
AI US 1998-114825 19980714 (9)
RLI Continuation-in-part of Ser. No. US 995150, now abandoned
PRAI US 1996-34095P 19961230 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Fredman, Jeffrey; Assistant Examiner: Chakrabarti, Arun Kr.
LREP Kilpatrick Stockton LLP
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 2014
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The present invention provides a method and a kit for the purpose of diagnosing a disease or determining the predisposition for a disease by measuring abnormalities in imprinting of a gene or population of genes. The disease that can be diagnosed by the present invention is selected from any disease that is mediated by, or is associated with, a particular gene or combination of genes that are subject to imprinting. According the present invention, the imprinting can be abnormally on or can be abnormally off. In those cases where the particular gene that is being examined is normally imprinted, but in the disease state is abnormally not imprinted, the present invention is designed to detect the "loss of imprinting" (hereinafter "LOI") thereby indicating that the disease may be present.

L7 ANSWER 5 OF 8 USPATFULL
AN 2000:101693 USPATFULL
TI Quality control system for monitoring and control of contaminants in recycled plastics
IN Tacito, Louis D., Merrimack, NH, United States
Marciniszyn, Adam, Epping, NH, United States
PA Plastics Forming Enterprises, Inc., Manchester, NH, United States (U.S. corporation)
PI US 6099659 20000808
AI US 1998-136716 19980819 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Gulakowski, Randy; Assistant Examiner: Chaudhry, Saeed
LREP Hayes, Soloway, Hennessey, Grossman & Hage PC
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 493
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A process for continuously discriminating between a contaminated plastic material containing trapped volatile contaminants and plastic material which contains an acceptable threshold of contaminants comprising first supplying a continuous source of plastic material wherein the plastic material contains trapped volatile contaminants and feeding a sample of the plastic material preferably to the input section of an auger conveyor. The auger conveyor contains a barrel and a transfer screw positioned within the barrel with flights thereon for conveying the plastic material, the auger also connected to an output section which itself is connected to a detector for detecting trapped volatile contaminants. Plastic material is then conveyed through said auger at a selected rate by rotation of the transfer screw and the auger is also heated to a selected temperature such that trapped volatile contaminants in the plastic material are removed therefrom and remain substantially within the flights and delivered to the detector. The apparatus and process herein is also configured in communication with a tracking database containing one or a plurality of programmable logic controllers (PLC's) which signal, divert and/or isolate **contaminated** recycled material from plastic material which contains an acceptable **threshold** of contaminants when the recycled material exceeds preselected **contamination** levels.

L7 ANSWER 6 OF 8 USPATFULL
AN 2000:95001 USPATFULL
TI Mixtures of dideoxy-nucleosides and hydroxycarbamide for inhibiting retroviral spread
IN Malley, Serge D., Villeurbanne, France
Vila, Jorge R., Lyons, France
PA The United States of America as represented by the Department of Health and Human Services, Washington, DC, United States (U.S. government)
PI US 6093702 20000725
AI US 1995-401488 19950308 (8)

RLI Continuation-in-part of Ser. No. US 1995-378219, filed on 25 Jan 1995, now abandoned which is a continuation-in-part of Ser. No. US 1993-169253, filed on 20 Dec 1993, now patented, Pat. No. US 5521161
DT Utility
FS Granted
EXNAM Primary Examiner: Tsang, Cecilia; Assistant Examiner: Crane, L. Eric
LREP Knobbe, Martens, Olson & Bear, LLP
CLMN Number of Claims: 8
ECL Exemplary Claim: 1,6
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 939
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method and composition for inhibiting the spread of a retrovirus such as HIV in a human cell population in which a retrovirus such as HIV is present has been found. The spread of the retrovirus is inhibited by treatment of the cells with a synergistic combination mixture of a dideoxy-ribonucleoside excluding AZT and hydroxycarbamide.

L7 ANSWER 7 OF 8 USPATFULL
AN 2000:87953 USPATFULL
TI Metal-containing ribonucleotide polypeptides
IN Wissler, Josef, Bad Nauheim, Germany, Federal Republic of
Logemann, Enno, Freiburg, Germany, Federal Republic of
Kiesewetter, Stefan, Lautertal-Unterlauter, Germany, Federal Republic of
Heilmeyer, Ludwig, Bochum, Germany, Federal Republic of
PA Fraunhofer-Gesellschaft zur Foerderung der Angewandten Forschung e.V., Germany, Federal Republic of (non-U.S. corporation)
PI US 6087123 20000711
WO 9704007 19970206
AI US 1997-794000 19970919 (8)
WO 1996-DE1337 19960717
19970919 PCT 371 date
19970919 PCT 102(e) date
PRAI DE 1995-19525992 19950717
DE 1995-19530500 19950818
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George C.; Assistant Examiner: Shibuya, Mark L.
LREP Marshall & Melhorn
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1319
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to bioactive ribonucleo polypeptides (RNP) containing copper, zinc or calcium. These are non-mitogenic morphogens for blood vessels of a defined primary structure for intercellular communication with genetic information. Zn/Ca/Cu-RNP can enzymatically hydrolyse nucleinic acids in a regulated manner (regulated nuclease activity) and be modulated and regulated via Zn/Ca/Cu-metal ion contents as "molecular switches" in mutual bioactivity. The compounds selectively stimulate the directional growth of the morphogenesis of blood vessels in vivo and in vitro and lead to neovascularisation of tissues. The invention further relates to a method of producing and obtaining the RNP as well as its utilisation, and medicines.

L7 ANSWER 8 OF 8 USPATFULL
AN 1998:36734 USPATFULL
TI Mixtures of DDI and D4T with hydroxycarbamide for inhibiting retroviral replication
IN Malley, Serge D., Villeurbanne, France
Vila, Jorge R., Lyons, France
PA Compagnie de Development Aguettant S.A., France (non-U.S. corporation)

PI US 5736526 19980407
AI US 1995-577322 19951222 (8)
RLI Division of Ser. No. US 1995-401488, filed on 8 Mar 1995 which is a continuation-in-part of Ser. No. US 1995-378219, filed on 25 Jan 1995, now abandoned which is a continuation-in-part of Ser. No. US 1993-169253, filed on 20 Dec 1993, now patented, Pat. No. US 5521161, issued on 28 May 1996
DT Utility
FS Granted
EXNAM Primary Examiner: Kight, John; Assistant Examiner: Crane, L. Eric
CLMN Number of Claims: 16
ECL Exemplary Claim: 1,9
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 874
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method and composition for inhibiting the spread of a retrovirus such as HIV in a human cell population in which a retrovirus such as HIV is present has been found. The spread of the retrovirus is inhibited by treatment of the cells with a synergistic combination mixture of a dideoxy-ribonucleoside excluding AZT and hydroxycarbamide.

=> d l7 8 kwic

L7 ANSWER 8 OF 8 USPATFULL
DETD . . . CD4, CD8 and .beta.2-microglobulin were quantified at days 0 and 90. p24 Ag, quantitative plasma and cell viraemia and RNA **PCR** were evaluated at days 0 and 90. For those patients for whom no virus was detectable by these methods, recovery. . .
DETD Particle-associated RNA in plasma was quantified with a **PCR** -RNA system: the **PCR** Amplicor HIV Monitor (Roche Diagnostic Systems (Sninsky J., Kwok S. The application of quantitative polymerase chain reaction to therapeutic monitoring.. . .
DETD Using the **PCR** RNA technique, plasma viral load was quantified in all patients before treatment, with values ranging from 3521 to 128973 copies per ml of plasma. At day 90, six patients showed no detectable viral load using the **PCR** RNA quantitative method. The viral load of the other six patients remained detectable but showed a substantial decrease of between. . .
DETD TABLE

Virological and immunological data at baseline and after three months' treatment with a combination of didanosine
and hydroxyurea

		PCR RNA	Detection of infectious virus		
CD4+	RNA copies/				
		*RNA Plasma	PBMC	.dagger.PBMC	
Age					
Risk					
Cells/mm.sup.3 (%)					
	ml plasma				
		detection			
		(TCID.sub.50.	.	.	det
		(-) 0	0	<1 0	(-)

H: homosexual. He: heterosexual. BS: bisexual. IDU: Intravenous Drug User AOC: accidental occupational **contamination**. non det: non detectable(sensitivity **threshold** = 200 RNA copies/ml). (%): CD4+ cells as
a percentage of total lymphocytes. *The symbols in brackets indicate the detection. . .

=> d l7 7 kwic

L7 ANSWER 7 OF 8 USPATFULL
SUMM . . . for Reagent Water 1970; Annual Book of ASTM-Standards, Easton Maryland, ASTM 1970. In addition it is freed of possible endotoxin **contaminations** by ultrafiltration on tenside-free membranes with an exclusion **threshold** of 10000 Daltons.
SUMM . . . or in vitro, which code the part sequences given according to claim 1, with at least 6 bases in the **PCR** reaction, or the antisense bioprocess technology.

=> d l76 kwic
L76 NOT FOUND
The L-number entered has not been defined in this session, or it has been deleted. To see the L-numbers currently defined in this session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> d l7 6 kwic

L7 ANSWER 6 OF 8 USPATFULL
DETD . . . CD4, CD8 and .beta.2-microglobulin were quantified at days 0 and 90. p24 Ag, quantitative plasma and cell viraemia and RNA **PCR** were evaluated at days 0 and 90. For those patients for whom no virus was detectable by these methods, recovery. . .
DETD Particle-associated RNA in plasma was quantified with a **PCR** -RNA system: the **PCR** Amplicor HIV Monitor (Roche Diagnostic Systems (Sninsky J., Kwok S. The application of quantitative polymerase chain reaction to therapeutic monitoring.. . .
DETD Using the **PCR** RNA technique, plasma viral load was quantified in all patients before treatment, with values ranging from 3521 to 128973 copies per ml of plasma. At day 90, six patients showed no detectable viral load using the **PCR** RNA quantitative method. The viral load of the other six patients remained detectable but showed a substantial decrease of between. . .
DETD TABLE

Virological and immunological data at baseline and after three months' treatment
with a combination of didanosine and hydroxyurea

		PCR RNA	Detection of infectious virus		
	CD4+	RNA copies/ * RNA			
			Plasma	PBMC	.dagger. PBMC
Age	Risk	Cells/mm.sup.3 (%)	ml plasma		
. . .	13324		non det (-)	0	0<1

(-)
H: homosexual. He: heterosexual. BS: bisexual. IDU: Intravenous Drug User AOC: accidental occupational **contamination**. non det: non detectable (sensitivity **threshold** = 200 RNA copies/ml). (%): CD4+ cells as a percentage of total lymphocytes. * The symbols in brackets indicate the
. . .

=> d l7 5 kwic

L7 ANSWER 5 OF 8 USPATFULL
AB . . . communication with a tracking database containing one or a plurality of programmable logic controllers (PLC's) which signal, divert and/or isolate **contaminated** recycled material from plastic

material which contains an acceptable **threshold** of contaminants when the recycled material exceeds preselected **contamination** levels.

SUMM . . . consumer which otherwise would be destined for disposal. This type of recycling has now become well known as post-consumer recycling (**PCR**), as opposed to recycling that develops as part of the reuse of by-products from a plastic manufacturing process (which by-products. . .

SUMM Unfortunately, the reprocessing and refabrication of **PCR** materials into useful products requires several steps (collection, handling/sorting, reclamation/cleaning and end-use fabrication) and presents unique problems. That is, each. . .

SUMM Not surprisingly therefore, and to assure consumer safety, regulatory agencies promptly became active with respect to the use of **PCR** material for food/beverage applications. For example, in 1992 the Food and Drug Administration published proposed guidelines for recycling, which divided. . .

SUMM . . . between levels of contamination derived from a given population of, e.g. PET containers. In other words, to the extent that **PCR** -PET flake has been analyzed for contaminants, it has been largely demonstrated on isolated portions of the flake, and not itself. . .

SUMM . . . is programmed to both identify and signal at a preselected contaminant levels, as well as acting to divert and isolate **PCR** plastic containing said selected and detected contaminant level from plastic material which contains an acceptable threshold of contaminants.

SUMM . . . further controls said recycling plant's reprocessing of recycled material such that said tracking database can signal, divert and/or isolate said **contaminated** recycled material from plastic material which contains an acceptable **threshold** of contaminant when said recycled material exceeds preselected **contamination** levels.

DRWD . . . plastic from a main recycling production line facility as combined with a PLC tracking database controller for signaling and diverting **PCR** plastic at selected **threshold** contaminant levels from non-**contaminated PCR** plastic.

DRWD . . . 2 is a block diagram flow-sheet further illustrating the invention herein as configured to simultaneously evaluate both unclean and cleaned **PCR** plastic material.

DETD As illustrated in FIG. 1, shown is an input section 10 wherein **PCR** material is continuously delivered to a chute 12 which contains a sampling system 14 for diverting a sample of said continuous source of **PCR** to detector apparatus 16. In preferred embodiment, detector apparatus comprises an auger conveyor 18 which contains a barrel and a. . .

DETD . . . control, the zone temperatures are set such that the temperature will be sufficient to drive trapped volatiles from the dirty **PCR** PET plastic, but not so high such that other material present in the flake (e.g., glue, or other lower melting. . .

DETD . . . does not indicate volatile contaminant levels below a preselected level (input at 26) is identified in FIG. 1 as "Accepted **PCR**" 36 for processing/cleaning into recycled "clean" flake.

DETD . . . noted, is a block diagram flow-sheet further illustrating the invention herein as configured to simultaneously evaluate both unclean and cleaned **PCR** plastic material. That is, bales of plastic for recycling are shown as entering the recycling facility at 38 followed by. . . and grinding and then at 40, being sampled in accordance with the illustration shown in FIG. 1. Accordingly, the accepted **PCR** material is stored at 42 followed by washing, a density separation treatment preferably accomplished by a sink/float or hydroclone treatment. . .

CLM What is claimed is:

. . . further controls said recycling plant's reprocessing of recycled material such that said tracking database can signal, divert and/or

isolate said **contaminated** recycled material from plastic material which contains said acceptable **threshold** of contaminants, when said recycled material exceeds a preselected **contamination** level.

13. A process for continuously discriminating between a contaminated plastic material containing trapped volatile contaminants and plastic material which contains. . . controlling said recycling plant's reprocessing of recycled material such that said tracking database controller can signal, divert and/or isolate said **contaminated** recycled material from plastic material which contains an acceptable **threshold** of contaminants when said recycled material exceeds a preselected volatile **contamination** level; c. conveying the sample of plastic material through said auger at a selected rate by rotation of said transfer. . .

=> d l7 4 kwic

L7 ANSWER 4 OF 8 USPATFULL

DRWD . . . the Apa I site), and B (with the Apa I site). Heterozygosity of genomic DNA was ascertained by performing DNA **PCR**, using primers 3 and 4 across the Apa I site, and the **PCR** product was digested with Apa I. Imprinting status was ascertained by performing RT-**PCR** on RNA, using primers 1 and 2 in exons 8 and 9, respectively. The cDNA **PCR** product, which is shorter than any possible contaminating genomic DNA product because of intron splicing, was electrophoresed and purified from an agarose gel. **PCR** was then performed using primers 3 and 4, end-labeling one of the primers. The **PCR** product was digested with Apa I, analyzed on a 6% polyacrylamide gel, and quantified on a PhosphorImager. The B allele is shorter but of equal radioactive intensity to the A allele. All RT-**PCR** experiments were performed in parallel in the presence and absence of reverse transcriptase, from the identical cDNA product, in order to rule out the presence of **contaminating** DNA. The **threshold** for scoring loss of imprinting (LOI) was less than a 3:1 ratio between the more abundant and less abundant alleles.. . .

DRWD . . . colon cancer patients. 3(A) Gene-specific cDNA, derived from reverse transcription with an IGF2 downstream primer, was amplified using promoter-specific primers. **PCR** products were subjected to Southern allele-specific hybridization (SASH) using allele-specific oligonucleotide probes, as described previously (He et al. (1998) Oncogene. . . by mixing cDNA homozygous for the A and B alleles at varying ratios, and then amplifying with promoter 4-specific primers. **PCR** products were detected by allele-specific oligonucleotide probe A or B respectively. The assay demonstrated that the amplification of promoter-specific cDNA. . .

DETD . . . samples which contain smaller numbers of cells and then enrich the cells. In addition, with certain highly sensitive assays (e.g., RT-**PCR** when IGF2 is abundant, and other methods like DNA methylation even when IGF2 not abundant) it is possible to get. . .

DETD . . . expression which rely upon the differential transcription of the two alleles, RNA is reverse transcribed with reverse transcriptase, and then **PCR** is performed with **PCR** primers that span a site within an exon where that site is polymorphic (i.e., normally variable in the population), and. . . 362:747-749; which teaches the assessment of allele-specific expression of IGF2 and H19 by reverse transcribing RNA and amplifying cDNA by **PCR** using new primers that permit a single round rather than nested **PCR**; Matsuoka et al. (1996) Proc. Natl. Acad Sci USA 93:3026-3030 which teaches the identification of a transcribed polymorphism in p57.sup.KIP2 ; Thompson et al. (1996) Cancer Research 56:5723-5727 which teaches determination of mRNA levels by RPA and RT-**PCR** analysis of allele-specific expression of p57.sup.KIP2 ; and Lee et al. (1997) Nature Genet.

15:181185 which teaches RT-**PCR** SSCP analysis of two polymorphic sites. Such disclosures are herein incorporated by reference. In this case, the biological sample will. . .

DETD . . . two alleles of the gene or genes for which the presence or absence of LOI is being measured. For example, RT-**PCR** followed by SSCP (single strand conformational polymorphism) analysis; restriction enzyme digestion analysis followed by electrophoresis or Southern hybridization; or radioisotopic **PCR**; **PCR**; allele-specific oligonucleotide hybridization; direct sequencing manually or with an automated sequencer; denaturing gradient gel electrophoresis (DGGE); and many other analytical. . .

DETD 3. Measuring the degree of relative transcription by RT-**PCR** of mRNA followed by a variety of detection schemes;

DETD . . . measuring the degree of LOI quantitatively by relying on the relative levels of transcription of the two alleles using quantitative **PCR** amplification, it is important to obtain high quality RNA. In this case, it is preferred to place the tissue in. . .

DETD . . . the degree of LOI quantitatively by a method which relies on the relative transcription of the two alleles, using quantitative **PCR** amplification, it is also important to avoid genomic DNA contamination of the cDNA, which is obtained from the mRNA. In addition, it is important to ensure linear amplification during any amplification step, e.g., polymerase chain reaction (**PCR**) amplification of the cDNA obtained from the mRNA. If the primers used in such a **PCR** amplification are exhausted, it is possible to obtain heterodimers of two different alleles, and any subsequent restriction enzyme digestion will. . . the restriction enzyme being used recognizes allele b, then the restriction enzyme cuts the bb' double helix. However, if the **PCR** amplification is allowed to progress to the point where the primers are exhausted, it is possible to obtain after the. . .

DETD . . . two alleles of the gene or genes for which the presence or absence of LOI is being measured. For example, RT-**PCR**, followed by gel electrophoresis to distinguish length polymorphisms, or RT-**PCR** followed by restriction enzyme digestion, or by automated DNA sequencing, or by single strand conformational polymorphism (SSCP) analysis, or denaturing. . . methods that exploit, for example DNA methylation (then there is no RT step, to convert RNA to cDNA prior to **PCR**).

DETD . . . to the two polymorphic alleles of the gene in question. Examples of such means include suitable DNA primers for the **PCR** amplification of the mRNAs corresponding to the two polymorphic alleles of the gene in question. Specific examples of such means. . .

DETD . . . alleles of the gene in question. Examples of such means include a sufficient quantity of suitable DNA primers for the **PCR** amplification of the mRNAs corresponding to the two polymorphic alleles of the gene in question, such that the **PCR** amplification may be carried out without exhausting the primers and linear amplification achieved. Specific examples of such means includes any. . .

DETD . . . (Rainier et al. (1993) Nature 362:747-749) that can be used to assess allele-specific expression by reverse transcription polymerase chain reaction (RT-**PCR**), of which 27 were heterozygous and thus informative for imprinting status analysis. Sixteen informative of 47 normal colon samples were. . .

DETD As described in the Results, many samples demonstrated substantial although incomplete loss of imprinting. A quantitative **PCR** assay (relative to the two alleles) was developed (also see FIG. 1). RNA samples were treated with DNase prior to. . . (CA).sub.n repeat polymorphism was used to analyze imprinting status of the gene. To exclude any possibility of genomic DNA contamination, **PCR** across an intron-exon boundary was first performed. For the Apa I polymorphism, primer Pla, located on exon 8, and primer P8b, on exon 9, were used to amplify cDNAs derived from reverse transcription. **PCR** was performed using the following conditions: 50 .mu.l of

reaction volume containing 2 .mu.l of cDNA template, at a final concentration of 0.5 FM each primer, 0.15 mM of dNTP, 1.5 mM of MgCl.sub.2, 1.times.**PCR** buffer (LTI), and 1.5 U of Taq polymerase (LTI). Thermal cycling was performed as follows: 94.degree. C. for 2 minutes;. . . for 1 minute, 52.degree. C. for 1 minute, 72.degree. C. for 1.5 minutes; and 72.degree. C. for 10 minutes. The **PCR**-amplified products were purified from 1.5% agarose gels, using a 123 bp ladder to identify the location of the cDNA (1224. . . genomic DNA contamination impossible. The cDNA fragments were purified using the Qiaquick gel extraction kit (Qiagen). A second round of **PCR** amplification was then performed using 1 .mu.l of purified first round **PCR** product as template, and primers P2 and P3, with P3 previously labeled using [.gamma..sup.32 P-ATP. The second round of **PCR** amplification was followed by 35 cycles of 94.degree. C. for 30 sec.; 55.degree. C. for 40 sec.; 72.degree. C. for 1.5 min.; and 72.degree. C. for 10 min. The **PCR** product (10 .mu.l) was digested in a 20 .mu.l volume with 20 U Apa 1, 10 mM NaCl, 3 mM. . . of the less abundant allele (0% representing monoallelic expression, 100% representing equal biallelic expression). Primers were maintained in excess over **PCR** product to avoid heterodimer formation. Control mixing experiments confirmed equal amplification of the two alleles, and the absence of heterodimer. . .

DETD IGF2 specific cDNA was made as described above. A semi-nested **PCR** approach was performed using promoter-specific primers to amplify transcripts derived from specific promoters as described previously (He and Cui, 1998). Duplicate **PCR** products were separated on 1.5% agarose gels, and the DNA fragments migrating at the predicted specific cDNA size were isolated. . .

DETD . . . markers for each sample: BAT-25, BAT-26, D2S123, D11S1318, D17S250, AP2, D11OS89, AP3, D18S58, D3S1283, D11S904, D11S1758, D11S4124, D11S860, and APC. **PCR** amplification was performed using 1 .mu.l of DNA (=0.15 .mu.g) in a final volume of 10 .mu.l, with a final concentration of 0.1 .mu.M each primer, 0.15 mM dNTP, 1.5 mM MgCl.sub.2, 1.times. **PCR** buffer (LTI), and 0.06 U Taq polymerase. In each case, one primer was end-labeled. **PCR** products were analyzed on 6% denatured polyacrylamide gels. The primer sequences were as described previously (Dietmaier et al. (1997) Cancer. . .

DETD . . . To confirm that biallelic expression was due to LOI and not to a shift in promoter usage to P1, promoter-specific RT-**PCR** was performed, using exon-specific primers (exon 3 for PI, exon 4 for P2, exon 5 for P3, and exon 6 for P4). The **PCR** products were then analyzed using allele-specific oligonucleotides as described (He et al. (1998) Oncogene 16:113-119), with reconstitution controls performed in. . .

=> d l7 2 kwic

L7 ANSWER 2 OF 8 USPATFULL

SUMM [0006] Due to their toxicity, safety **threshold** values have been recommended for DON mycotoxin **contamination** in grain used for human food and animal feed. (Van Egmond, 1989, Food Addit Contam. 6:139-188; Underhill, CFIA Fact Sheet,. . . effects of mycotoxins on poultry and cattle are less quantified since both of these species are less sensitive to DON **contamination** in their feed, and detailed economic **threshold** assessments have not been made.

DETD . . . 5). The Rpl3-specific sequence was amplified using primers CRPL31104L and CRPL33U (5'-GTCGCACAGGAAGTTCGA)(SEQ ID No.: 6) using the Expand High Fidelity **PCR** System (Boehringer Mannheim). **PCR** products were ligated into the pGEM-Teasy vector (Promega) overnight at 4.degree. C. and transformed into electrocompetent DH5.alpha. cells. Sequencing was. . . a commercial Licor sequencing service and sequences were compiled and analysed in a Lasergene DNAStar

DNA analysis program. The sequenced RT-**PCR** clones fell into two classes of cDNA, represented by maizel (SEQ ID No.: 7) and maize2 (SEQ ID No.: 8). . .

=> d l7 2 5

L7 ANSWER 2 OF 8 USPATFULL
AN 2002:166386 USPATFULL
TI Tolerance of trichothecene mycotoxins in plants through the modification of the ribosomal protein L3 gene
IN Harris, Linda J., Greely, CANADA
Gleddie, Stephen C., Ottawa, CANADA
PA Ministry of Agriculture (non-U.S. corporation)
PI US 2002088022 A1 20020704
AI US 2000-725957 A1 20001130 (9)
RLI Continuation-in-part of Ser. No. US 2000-567326, filed on 9 May 2000, ABANDONED Continuation of Ser. No. US 1997-909828, filed on 12 Aug 1997, GRANTED, Pat. No. US 6060646
DT Utility
FS APPLICATION
LN.CNT 908
INCL INCLM: 800/279.000
NCL NCLM: 800/279.000
IC [7]
ICM: A01H005-00

L7 ANSWER 5 OF 8 USPATFULL
AN 2000:101693 USPATFULL
TI Quality control system for monitoring and control of contaminants in recycled plastics
IN Tacito, Louis D., Merrimack, NH, United States
Marciniszyn, Adam, Epping, NH, United States
PA Plastics Forming Enterprises, Inc., Manchester, NH, United States (U.S. corporation)
PI US 6099659 20000808
AI US 1998-136716 19980819 (9)
DT Utility
FS Granted
LN.CNT 493
INCL INCLM: 134/019.000
INCLS: 134/010.000; 134/017.000; 209/001.000; 209/002.000; 209/003.100; 209/011.000
NCL NCLM: 134/019.000
NCLS: 134/010.000; 134/017.000; 209/001.000; 209/002.000; 209/003.100; 209/011.000
IC [7]
ICM: B08B007-00
ICS: B03B001-02
EXF 134/17; 134/19; 134/10; 134/15; 134/23; 209/1; 209/2; 209/3.1; 209/11; 209/552
CAS INDEXING IS AVAILABLE FOR THIS PATENT.